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1381	ATGT	TCC	~~~	ACA								AGT		VCG1							1440
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	AGCI	CGA	CGA	GA1	CIC	TG	TII	У¢	TG	GA	AAA	CIG	SAAC	CTC	TC	STG	TTT	ATT	ATA	ATC	
1441			+				-+			-+-							-+-			+	
	L	D	E	M	C	D	150	_													
	TIGO	TTA	AAC	TTO	-24	CTC				·CT	TTC	TAC	acc.		: 10	CTG	CAT	ccc	CAA	AAT	
1501																					1560
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1561	CAG						-+			LAT	CTG	ACC.	AAC:	TTA:	TTG						1.620
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	TATO	TGA	ATC	TAC	CGG	ATC	TC	TT	TA	AT1	CAG	AAA	TTA	TGA:	TTC	AAT	CGT	TTG	GCI	CAA	
1621			+				-+			+				+			-+-			+	1680
												N	Y	D	S	I	V	W	L		
	AGA:	- N - T	,		· ·	TCC:		~~~	P & C 1	. ~~	x	~~~	እ ጥጥ	T 2 C	x	T 2 F	***	~~	19	-	
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	K	•																			
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1801												TTC					-			TGT	1860
1861				+			-+-			+				+							1920
			Ą	n2	273																
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			LAG	AAG	CGA	AGA	CGA	ICT	TCT	CAA	TTI	ccc	ATC	GGT	GGA	.GC?	\TG1	CAC	CCT	CAGT	
1921				+ s	 Е	 D	-+-			+ N				+			+-				1980
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	TGT.	ACTO	CAA	AAG	GAT	фт	AAG	TTG	CTT	GCC	GAT	TCT	GGT	ACA	ATA	TCI	CTA	LAT:	TAT:	I GGT	
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2041		•		+			-+-							+			+-				2100
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2101						-		-													2160
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				GAA	LATA	TCA	AAT	GCI	GCI	TCI	CA	VAC	\TGC	GA)	TTC	:AT	IGA			ATCA	
2161				+			-+-				+			+			+			+	2220
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FIGURE 1

2221	II	GGA	AA1	(DD	TG	ATC	TT	ATG/	ATTI	TCI	AG/	AAG	CTT	ATG	GAA:	rgc	CGA	TGC	CIG	TTGG	\ ► 2280
	L	E		D				D	F 300					G		P	P 14		V 310		
2281														 	GCAC		Gλλ			CAACO	; - 2340
	-	ĸ	_		D			:	320							þ	intr	on			
2341				+-					ETGA		+			+			GAG	TGG +	GAC	ATACO	2400
2401	TG	 ATT	GIO	TT:	LAA?	ATT:	TAC	AAT:	TTAT	AGC	ATC	CAA	AAI	CAA	GAA:	T.		TCC	TGG	CACG	+ 2460 A
	GA	GAA 	AAC	TG	CT	AGC:	TAC	GT/	ACC	GAC	AG.	ATT	TTC	TIG.	ATA:	III	GCC	ATC	GAT	TAA:	2580
2581	GA.	 Aat	TT	+- LTT/	NAA:	IGA/	AAG		STA:	rgac	-+-	IGT	 TTT	CAT	TAT:	TTI	TCG	ATT	TIC	CTT	2640
	TT	GTI	TC:	TTT:	TA:	TTT	AAA	GCC:	TTT:	TAT1	TTC	SAA	ACA	AGT	CTA	A	KTA.	KTTA	AAA	ACTG	2760
	CT		TA	+	CGG		ACT	+	 !TT/	ATTI	AA:	ICA	 TTT	TCC	 GGλ	ATG	TCG	.+ :AAA	CGA	AATA	2820
2881	TA	CAT	TT	TAC	STC	CAA	AAT	+:	TAGO	STA1	AT:	rct 	TAA AGG	AAT + ATT	TATO 	CGC	ACA	TGA	TGC:	TATC	A 2940
2941		 M		Q 340	L	N	N	K	L	Ē			G						c		1 2000
3001			Y	s				+			-+-			+				+		STCAC	3060
3061			GA:																	ACCC	3 + 3120
3001			D	R 380	s.	A ′	L,						M		₽					P 1	
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				100										410 In	tro	n (5		•	L I	
3181		D	E	V 120	λ	D	R	+	ĸ	R	L	 S	ĸ	+				+			3240
3241				+·		TTA					G			+				+	м	P 1	+ 3300

FIGURE 1

301	T	TI	GA	ΞX.	TTC	CAJ	W.	AT?	ľGλ	TC		ATT				TC	TT	CT:	rg,	W	ĊA	CG1	rcg +	TT 	GA1			3360
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361		CI C		CG 	+-	_						GTC									TT	AA.	ATT +	TI	CAC	AA N		3420
3421																									GT			3480
	G	I	S		I		47		Q	R		L	L	E	1		G	N	. 1		N 30	V	S	•	V	P		
3481	GA	GC(3AC			AC			NC!																AT			3540
	E	R	Ħ	i	I	-	50	-	H	F	•	Q	K	F	1	R	R	S		-	A	S	E	:	M	Y		
3541					+-									-+-				+					+					3600
	P CA		_		T TI	_	52 32	20	T CT			I :AA								5	30		_		STG		CA	•
3601	H				+-			D		+		ĸ		-+-				+										3660
	AT	ΆŢ	TGC	:C1	GI	TA:	54 :A:	TC	CC	CTC	:GA	AA'	TAG	CG1	TT	AT.	AC'	ITI	TT	CG	CAC	GA	GT	rt'	TCT	CA	TT	3720
	TI	TT								TA:	TT:	CT	CT	CCA	(AA	AT	TT	CAG	AT	CI	ATC	CCC		AT	STT	CT	TA	3780
3721	A	AT				TI	T	CTA	CA	-										TC	TC	ATC	CT	TG	CTT	TT	TT:	T .
3781	TI					AT1	rc.	AG1	TT	t-	rT?	TAT	Aλ	TT:						AT	TA	ATA	CA'	TT	CAC	GT	AA	3840
3841	AC														CA	AA	IG	AT?	TA	TT	CC	CTA		GT	TCG	AΑ	AC	3900
3901																								TT	AGI	CI	CC	
3961						AA(ST			-		IGI							IGC					GG	ACA	TT	TG	
4021						AC	GA	AA)	ACC	+- GI	AA:	 III	Ť-	AC	 RAI	TI	cc	TT							GTI			4080
4081					-+ TC	TG:	 TŤ	ĞG	 CG1	+- 'CA	 TT	 AC1	 :AC												GAC			4140
4141					-+					+-				-+					+			~	-+-				+	4200
4201					-+					+-				-+					+				-+-				+	4260
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4321	_				-+					+-		CA:		-+					+- -				-+-				+	4380
4301														44	07													

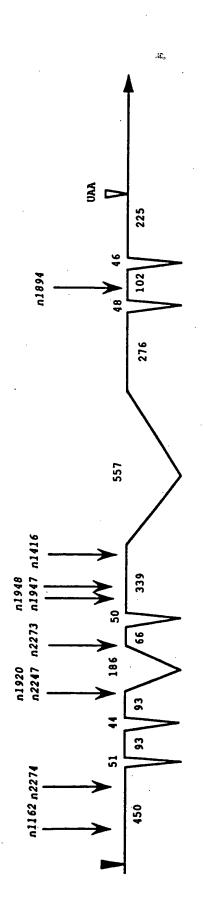


FIGURE 2

	10 <u>X</u>	,	12 Y		14 Z				18 ·X			21 <u>·Z</u>
Calcium-binding loop consensus	D		N D		S N D				TSEQDN	•		Ē
EF-hand consensus	٥	*	0	*	0	G	*	*	0	*	*	E
ced-4 sequence 1	¥	N	N	Q	S	H	L	A	D	F	L	E
sequence 2	<u>s</u>	L	E	I	D	E	С	Y	D	F	L	E
Parvalbumin (carp) (hake) (ray)	D	Q.	D	K	D	D	F	I	G	Ε	D D D	E
SCBP (Amphioxus I)	D	I	N	K	D	D	v	v	s	W	E	E.
ICaBP (bovine)	A D	K	E N	G G	D D	P G	Q E	V L	s	K F	E	E
Troponin C (rabbit)	D D	E R	N D	G A	S	G G	T Y	I I	D D	F A	KEED	E E
Calmodulin (bovine)	D	ĸ	D	G	N	G	T	I	T	T	ĸ	E
Trypsinogen	L	G	E	D	N	I	N	V	Æ	G	N	E
Fibrinogen	D	N	D	N	D	K	F	E	3N	С	A	E
Villin	G	V	D	P	S	R	K	E	N	Н	Ĺ	s
GBP	D	L	N	K	D	G	Q	I	Q		I	E

ced-3 Genomic Sequence

	JACTG1
TTTAGCACAATTAATCTTGTTTCAGAAAAAAAGTCCAGTTTTCTAGATTTTTCCG	+ STCTTA
TTGTCGAATTAATATCCCTATTATCACTTTTTCATGCTCATCCTCGAGCGGCACG	STOCTO
AAAGAATTGTGAGAGCAAACGCGCTCCCATTGACCTCACACTCAGCCGCCAAAA	
GTTCGAACATTCGTGTGTTGTGCTCCTTTTCCGTTATCTTGCAGTCATCTTTTGT	+
	+
TTTTCTTTGTTCTTTTTGTTGAACGTGTTGCTAAGCAATTATTACATCAATTGAA	+
GGCTCGCCGATTTATTGTTGCCAGAAAGATTCTGAGATTCTCGAAGTCGATTTTA	+
TTTAACCTTGGTTTTTGCATTGTTTCGTTTAAAAAAACCACTGTTTATGTGAAAA	ACGAT
TAGTTTACTAATAAAACTACTTTTAAACCTTTACCTTACCTCACCGCTCCGTGT	TCATG
GCTCATAGATTTTCGATACTCAAATCCAAAAATAAATTTACGAGGGCAATTAATG	STGAAA
CAAAAACAATCCTAAGATTTCCACATGTTTGACCTCTCCGGCACCTTCTTCCTTA	AGCCCC
ACCACTCCATCACCTCTTTGGCGGTGTTCTTCGAAACCCACTTAGGAAAGCAGTG	+ STGTAT
	+
	+
	+
SATCAGGAGCTTTCAGGGTAAACGCCCGGTTCATTTTGTACCACATTTCATCATT	+
GTCGTCCTTGGTATCCTCAACTTGTCCCGGTTTTGTTTT	+
ACCTGTCTCCGTCTCAATTATCGTTTAGAAATGTGAACTGTCCAGATGGGTGAC	CTCATA
TGCTGCTGCTACAATCCACTTTCTTTTCTCATCGGCAGTCTTACGAGCCCATCA	TAAAC
TTTTTTTCCGCGAAATTTGCAATAAACCGGCCAAAAACTTTCTCCAAATTGTTA	CGCAA
ATATACAATCCATAAGAATATCTTCTCAATGTTTATGATTTCTTCGCAGCACTT	TCTCT
CGTGTGCTAACATCTTATTTTATAATATTTCCGCTAAAATTCCGATTTTTGAG	TATTA
ATTTATCGTAAAATTATCATAATAGCACCGAAAACTACTAAAAAATGGTAAAAGCT	CCTTT
Repeat 1	
CARACTER AGAGA TOTALA GAS ATTALES TATALAS AS TOTALAS AS	TGCGC
	TGCGC
lacatatttgacggcaaaatatctcgtagcgaaaactacagtaattctttaaatg	ACTAC
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GCT.	ACG	GAT	ATT	TTO	CGC	CGC	CAA	ATA	TGA	CTG:	TAA:	CACC	CAT	TC	гст	GAA'	ידדי	rgt	GTT
TCC	GTA	TAA	TTT	CAC	AAC	-+- 3AT'	TTT	GGC.	TTC	CCA	CTT	 TAA2		GC		-+- -GA'	 rtt:	 TT	+
		TCG				-+-			+			+				-+			+
		+				-+-			+			+				-+			+
		AAA: +				-+-			+-			+				-+			
TTC	CAGO	CTG	ACA	AAC	AGA	-+-	CAA	AAA	CAC	AAC	AAA	TTA:	TTA	AA	ATC	AG:	TTT:	CA	AAT
raaj	VAAI	AAC	GAT	TTC	TC	TT	GAA.	AAT'	TGT	GTT?	TA?	GTI	TGC	GAJ	LAA1	'AA	AG	GA	АСТ
GAT:	CAA	LAAC	AAT	TTT	AAC	:AA	AAA	AAA	ACC	CAZ	LAA!	TCG	CCA	GAZ	ATC	:AAC	AT		. A A
rtc	VAGA	GGG	TCA	AAA	TTI	TC	CGA:	TTT'	rac:	rgac	CTT	CAC	CTI	TT	TTT	CG	'AG	TC	+ AGT
CAG	STTO	TTG	 GAG	 TTT	TTC	+-	GAA	AAC	+· FAG	GAAZ	AAA	ATC	GAT			-+			+
		TTT				-+			+-			+				+			+
		+				+			+-		-AC	+			LATA	AT:	TC	ACTO	CAT
÷:																			
TTC	CAGA	CTA	AAT	CGA	AAA	TC	AAA:	rcg:	rac:	CTC	SACT	`ACG	GGI	CAC	TAC	AG	.GG	CAI	ACC
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		GAA				+			+- R	s	L	+	E		N N	+		rga: M	+
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TG	AAG	TGA	AAT	ATA:	TTT:	TATT	'TAC'	TGA	AA	GCT(CGA	GTG	ATT	ATT	TAT	TTTI	[TA]	ACA	CTA
			-			-+ GCCA													
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TG	TCC	AAT	GTC.	ACC	GGC:	AAGO	CAT	CGI	CG	GAG	CCG	CGC	ATT	'GAG	ccc	CGC	CGG	CTA	CAC
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TC	ACC	GAC	CĆG	AGT'	TCA	CCGI	GAC	AGC	CGT	CTC	TTC	AGT	GTC	ATC	ATT	CAC	TTC'	TTA	TCA
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				lepe															
AAC	ACT					1 TGC													
		'AAA'	TTC	TGA	GAA		GCAI	TA	СТС	AAC	AT	ATTI	GAC	CGCC	CAZ	ATA	TCT	CGI	AGC
		'AAA'	TTC	TGA	GAA	TGC	GCAI	TA	СТС	AAC	AT	ATTI	GAC	CGCC	CAZ	ATA	TCT	CGI	AGC
		AAA	TTC	TGA	GAA	TGC	GCAT	TA	CTC	AAC	ATA	ATT	GAC	GCG	CA	ATA -+-	TCT	CGI	AGC
GA?	AAA/	AAA	TTC +	TGA	GAA	TGC	GCAT	TAC	CTC + TAT	TGI	ATA	TGT	GAC	TTT	CAZ	ATA -+- GCT	TCT	CGI	TAGO
GA?	AAA/	AAA	TTC +	TGA	GAA	TGC	GCAT	TAC	CTC + TAT	TGI	ATA	TGT	GAC	TTT	CAZ	ATA -+- GCT	TCT	CGI	TAGO
GAZ	AAAZ	AAATAC	ATTC	TGA	CCT	TGC	AATO	AC	CTC + TAT +	TGI	ATA	rgro	CGA	rtt,	ACG	GGCT	TCT	TTT	TAGC
GAZ	AAA/	TAAA	ATTO	TAAC	CCT	TGC	AATO	ACA	CTC + TAT +	TGI	AG	TAA:	GAC	TTT	ACGG	GCT	CGA	TT	TAGC
GAZ	AAA/	TAAA	ATTO	TAAC	CCT	TGC	AATO	ACA	TAT	TGT	TAG	TAA:	TTTC	TTT#	ACGO	GCT	CGA	TTT	TAGC
GAZ	AAAZ	AATA	ATAT	TAAC	CCT	TTA	AATO	GACA	CTC + TAT +	TGI	TATA	rGT(TTTC	TTT	ACG	GCT	CGA	TTT	TAGO
GA/	ACG	AAATA	TTTC	FAAC	CCGA	TGC	AATC	TACAACA	CTC+ TAT+ ACG+	TGI	TAG:	TAA:	TGAC	GTC	ACGO	GGCT	TCT	TTT	TAGO
GAZ	ACG	AAATA	TTTC	FAAC	CCGA	TTA	AATC	TACAACA	CTC+ TAT+ ACG+	TGI	TAG:	TAA:	TGAC	GTC	ACGO	GGCT	TCT	TTT	TAGO
GAZ	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	ATAC	TTTC	######################################	CCC	TTA	AATC	ACA	CTC+ TAT+ ACG+ ATT+	TGT	CATI	TAA:	TTTTC	GTC.	ACGC	TTTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	TCT	TTT	TAGC

Repeat 2

	Repeat 2	
	TTTTTTCATTCAAGATATGCTTATTAACACATATAATTATCATTAATGTGAATTTCTTG	
L		354
	TAGAAATTTTGGGCTTTTCGTTCTAGTATGCTCTACTTTTGAAATTGCTCAACGAAAAA	
		360
Ļ	TCATGTGGTTTGTTCATATGAATGACGAAAAATAGCAATTTTTTATATATTTTCCCCTAT	366
L	TCATGTTGTGCAGAAAAAAAAGCGCATGCATTTTTTGACATTTTTACATCGA	372
. `	ACGACAGCTCACTTCACATGCTGAAGACGAGAGACGCGGAGAAATACCACATCTTTCT	378
	Repeat 2	
	GCGTCTCTCGTCTTCAGCATGTGAAATGGGATCTCGGTCGATGTAAAAAAATGTCGAATA	384
		1
	ATGTAAAAATĠCATGCGTTTTTTTACACTTTTCTGCACAAATGAATAGGGGGAAAATGT	390
		390
	ATTAAAATACATTTTTTGTATTTTTCAACATCACATGATTAACCCCATTATTTTTTCGTT	20
		396
	GAGCAACTTAAAAAGTAGAGAATATTAGAGCGAAAACCAAAATTTCTTCAAGATATTACC	
•		402
	TTTATTGATAATTATAGATGTTAATAAGCATATCTTGAATGAA	
	GCGAAACACCTGAAAAAAATCAAAAATTCTGCGAAAATTGAAAAAATGCATTAAAATACA	408
•	TTTTTGCATTTTTCTACATCACATGAATGTAGAAAATTAAAAGGGAAATCAAAATTTCTA	414
	GAGGATATAATTGAATGAAACATTGCGAAATTAAAATGTGCGAAACGTCAAAAAAGAGGA	426
- 2	TO THE TOTAL PROPERTY OF THE P	

	G	С	S	S 19	O L	G	Y	s	S	s	R	N	R	s 20	F	s	Ķ	A	s
TGC	SACC	AAC	TCA	ATA	CAT	ATT	CCA	TGA	AGA	GGA	TAT	GAA	CTI	TGT	CGA	TGC	ACC	AAC	:CA
G	P	T	Ω	Y 21	o I	+ F	н	E	-+- E	D	M	N N	F	V 22	D	+ A	P	T	-+ I
CAA	CCG	TGT	TTT	CGA	CGA	GAA	AAC	CAT	GTA	.CAG	AAA	CTI	CTC	GAG'	TCC	TCG	TGG	AAT	GT
 s	 R	+ V	 F			+ K			-+- Y		 N	+ F				+			-+
			_	23	_			••	•	• `	••	•	3	24	-			m	С
CC1	CAT	CAT	AAA	TAA	TGA	ACA	CTT	TGA	GCA	GAI	GCC	AAC	ACG	GAA:	TGG	TAC	CAA	GGC	CG
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LCAA	GGA	CAA	TCT	TAC	CAA	TTT	GTT	CAG	ATG	CAT	GGG	СТА	TAC	GGT	TAT	TTG	CAA	GGA	CA
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TCT	'GAC	GGG. +	AAG 	GGT.	ACG	GCG.	AAA	TTA	TAT	TAC	CCA	AAC	GCG	AAA:	rtt.	GCC.	ATT	TTG	CG
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CGA	AAA'					rcT	CGA	CAC	GAC.	AAT	=== TTG	=> TGT	TAA	ATG	CAA	AAA'	TGT	ATA	ΑT
		TGT	GGC	GCC	CGG	+			-+-			+				+			-+
TTG	CAA	TGT	GGC	GCC AAA	CGG	FGA.	ACT	rcc	-+- GCG -+-	 AAA	ATG	+ ATT +	TAC	CTAC	: 3TT:	+ TCG: +	AAA'	 TTT	-+ TC -+
TTG	CAA	TGT AAA ACCG	GGC ACA GCT	GCC AAA'	CGG	FGA FGT	ACT	TCC	-+- GCG -+- ICT	AAA TAG	ATG	+ ATT + TTC	TAC	CTAC	STT	TCG; + TGA	AAA'	TTT	-+ TC -+ AA
TTG	CAA	TGT AAA ACCG	GGC ACA GCT	GCC AAA'	CGG	FGA FGT	ACT	TCC	-+- GCG -+- ICT	AAA TAG	ATG	+ ATT + TTC	TAC	CTAC	STT	TCG; + TGA	AAA'	TTT	-+ TC -+ AA
TTT	TTT	TGT(GGC ACA GCT AAT	GCC AAA'	CGG	FGA	ACT	TCC	GCG.	TAG	ATG	+ ATT TTC + AAC +	TAC TAT.	CTAC	STT	TCG.	AAA' TGT	TTT AAA CAA	TC -+ AA -+ TT
TTT	TTT(TGT	GGC ACA GCT AAT	GCC AAA' ACA'	CGG	rga rgt rgt Aca rcc	ACT GTT ATT	TCC TTT'	GCGC	TAG ATA	ATG	+ ATT TTC + AAC +	TAC TAT. TTG.	AATA	STT:	TCG. TGA' TGA' TGA'	AAA TGT: AAT	TTT AAA CAA	TC -+ AA -+ TT -+ AC
TTTG	TTTO	TGT(GGC ACA GCT AAT TCA	GCC AAA' ACA' TTTG	CAG	rga rgt ACA rcc rcc	ACT	TTC:	GCG TCT CGC GCA GCA	TAG	ATG TTT CAA TTT	+ ATT + AAC + AAA	TAC TAT	AATA	GTT	TCG. TGA: CGA: H AAT:	AAA' AATG	TTT AAA CAA	TC -+ AA -+ TT -+ AC -+ AA
CTTG CCG TCT GTG	TTT(TGT(AAA) CCG(CCG(CCG(CCG(CCG(CCG(CCG(CCG	GGC ACA GCT AAT	GCC AAA' ACA' TTT' AAA' GAA	CAG	rga rgt rgt ACA rcc rat rat	ACT ATT	TCC TTC AATC	GCG. CGC. GCA	TAG ATA CAA CTT	TTT	ATT TTC AAC AAA AAA	TAC TAT. TTG. ATT	ATAC	GG/	TCGA TGA TGA TGA TGA TGA TGA TGA TGA TGA T	AAA TGT AAT TGG AGC	TTT AAA CAA CAA AAT	-+ TC -+ AA -+ TT -+ AC -+ AA -+ IG
TTTG CCG TCT GTG	TTTC	TGT	GGC ACA GCT AAT TCA TATO	GCC AAA TTT AAA GAA	CAG	TGT	ATT	TCC TTC AATC	GCG. CGC. GCAC	TAG	TTT.	+ ATT + AAC + AAA + AAA	TAC TAT. TTG. ATT	CTAC	GGA TTC	TCGA TGA TGA TGA TGA TGA TGA TGA TGA TGA T	AAA'	CAA CAA	-+ TC -+ AA -+ TT -+ AC -+ AA -+ TG -+
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ATGTANACTGATATTCACAGANANACCAGANANATTCCCAGCCTTGTTCCT ATGTANACTGATATTTAATTTCCAGGGANTGCTCCTGACAATTCGAGACTTTGCCAAAC G M L L T I R D F A K H 290 CGAATCACAGGGAGATTCTGCGATACTCGTGATTCTATCACACGGAGAAGAGAATGTGA E S H G D S A I L V I L S H G E E N V I 310 TATTGGAGTTGATGATATACCGATTAGTACACACGAGATATATGATCTTCTCAACGCGG I G V D D I P I S T H E I Y D L L N A A 330 A(n2) ANATGCTCCCCGTCTGGCGAATAAGCCGAAAATCGTTTTTGTGCAGGCTTGTCGAGGCG N A P R L A N K P K I V F V Q A C R G E 350 TTCGTTTTTTATTTTAATTTTAATATAAATATTTTAAATAAA		CAA	TTT	TCT	GCA	AAA	TAC	CAA	AAA	GAA	ACC	CGA	AAA	AAT	TTC	CCA	GCC	TTC	TTCC
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D N G F P V L D S V D G V P A F L R R G ATGGGACAATCGAGACGGGCCATTGTTCAATTTTCTTGGATGTGTGCGGCCGCAAGTTC W D N R D G P L F N F L G C V R P Q V Q 390 400 I intron 6 GGTTGCAATTTAATTTCTTGAATGAGAAATATTCCTTCAAAAAAATCTAAAATAGATTTTT TTCCAGAAAGTCCCGATCGAAAAAATTGCGATATAATTACGAAATTTGTGATAAAATGAC Repeat 4 AACCAATCAGCATCGTCGATCTCCGCCCACTTCATCGGATTGGTTTGAAAGTGGGCGGA	TC	~~~	m.c.c	, 3 mm	~~~														
TATGGGACAATCGAGACGGCCATTGTTCAATTTTCTTGGATGTGTGCGGCCGCAAGTTC W D N R' D G P L F N F L G C V R P Q V Q 390 400 ! intron 6 GGTTGCAATTTAATTTCTTGAATGAGAATATTCCTTCAAAAAAATCTAAAATAGATTTTT TTCCAGAAAGTCCCGATCGAAAAAATTGCGATATAATTACGAAATTTGTGATAAAATGAC Repeat 4 AACCAATCAGCATCGTCGATCTCCGCCCACTTCATCGGATTGGTTTGAAAGTGGGCGGA			+			AG1	+		TTC	TGT -+-			AGT +	TCC	TGC 	ATT	TCT	TCG	TCGT
ATGGGACAATCGAGACGGGCCATTGTTCAATTTTCTTGGATGTGTGCGGCCGCAAGTTC W D N R' D G P L F N F L G C V R P Q V Q 390 400 intron 6 GGTTGCAATTTAATTTCTTGAATGAGAATATTCCTTCAAAAAAATCTAAAATAGATTTTT TTCCAGAAAAGTCCCGATCGAAAAATTGCGATATAATTACGAAATTTGTGATAAAATGAC Repeat 4 AACCAATCAGCATCGTCGATCTCCGCCCACTTCATCGGATTGGTTTGAAAGTGGGCGGA	Ď	N	G	F	P	V	_	_	s	v	D	G	V	P	A	F			R C
ATGGGACAATCGAGACGGGCCATTGTTCAATTTTCTTGGATGTGTGCGGCCGCAAGTTC W D N R' D G P L F N F L G C V R P Q V Q 390 400 intron 6 GGTTGCAATTTAATTTCTTGAATGAGAATATTCCTTCAAAAAAATCTAAAATAGATTTTT TTCCAGAAAAGTCCCGATCGAAAAATTGCGATATAATTACGAAATTTGTGATAAAATGAC Repeat 4 AACCAATCAGCATCGTCGATCTCCGCCCACTTCATCGGATTGGTTTGAAAGTGGGCGGA							37	0	:								38	0	
W D N R' D G P L F N F L G C V R P Q V Q 390 400 intron 6 GGTTGCAATTTAATTTCTTGAATGAGAATATTCCTTCAAAAAAATCTAAAATAGATTTTT TTCCAGAAAGTCCCGATCGAAAAATTGCGATATAATTACGAAATTTGTGATAAAATGAC Repeat 4 AACCAATCAGCATCGTCGATCTCCGCCCACTTCATCGGATTGGTTTGAAAGTGGGCGGA																			3
W D N R' D G P L F N F L G C V R P Q V Q 390 400 intron 6 GGTTGCAATTTAATTTCTTGAATGAGAATATTCCTTCAAAAAAATCTAAAATAGATTTTT TTCCAGAAAGTCCCGATCGAAAAATTGCGATATAATTACGAAATTTGTGATAAAATGAC Repeat 4 AACCAATCAGCATCGTCGATCTCCGCCCACTTCATCGGATTGGTTTGAAAGTGGGCGGA			CAA	TCG	AGA	CGG	GCC.	ATT	GTT	CAA	TTT	TCT	TGG	ATG	TGT	GCG	GCC	GCA	 ከተሞር
390 400 intron 6 GGTTGCAATTTAATTTCTTGAATGAGAATATTCCTTCAAAAAAATCTAAAATAGATTTTT TTCCAGAAAGTCCCGATCGAAAAATTGCGATATAATTACGAAATTTGTGATAAAATGAC Repeat 4 AACCAATCAGCATCGTCGATCTCCGCCCACTTCATCGGATTGGTTTGAAAGTGGGCGGA	ATG	NOO					-												
GGTTGCAATTTAATTTCTTGAATGAGAATATTCCTTCAAAAAATCTAAAATAGATTTTT TTCCAGAAAGTCCCGATCGAAAAATTGCGATATAATTACGAAATTTGTGATAAAATGAC Repeat 4 AACCAATCAGCATCGTCGATCTCCGCCCACTTCATCGGATTGGTTTGAAAGTGGGCGGA			+	;			T —			-+-			+				+		,
Repeat 4 AACCAATCAGCATCGTCGATCTCGCCCACTTCATCGGATTTGTAAAGTGGCCGAAATTTGTGAAAGTGGCCGAAATTTGTGAAAGTGGCCGAAATTTGTGAAAGTGGGCGGAAACCAATCAGCATCGTCGATCTCCGCCCACTTCATCGGATTTGAAAGTGGGCGGAAACCCAATCAGCATTGATTG			+	R [/]	Ď	G	_	_	F	-+- N	F	L	G G	С	v	R	_	_	· V (
TTCCAGAAAGTCCCGATCGAAAAATTGCGATATAATTACGAAATTTGTGATAAAATGAC Repeat 4 AACCAATCAGCATCGTCGATCTCCGCCCACTTCATCGGATTGGTTTGAAAGTGGGCGGA	W	.D	+ N on	6		-	39	0			_						40	0	•
Repeat 4 AACCAATCAGCATCGTCGATCTCCGCCCACTTCATCGGATTGGTTTGAAAGTGGGCGGA	W I i	.ntr	On AAT	6 TTA	ATT	TCT'	39 TGA	O ATG	AGA	ATA'	TTC	CTT	CAA	AAA	ATC	TAA	40 AAT	0	•
AACCAATCAGCATCGTCGATCTCCGCCCACTTCATCGGATTGGTTTGAAAGTGGGCGGA	W I i	D .ntr	on AAT	6 TTA	ATT	TCT	39 TGA	O ATG	AGA.	ATA'	TTC	CTT	CAA +	AAA 	ATC	TAA	AAT	o AGA	TTTTT
AACCAATCAGCATCGTCGATCTCCGCCCACTTCATCGGATTGGTTTGAAAGTGGGCGGA+	W I i	D .ntr	On AAT	6 TTA GTC	ATT CCG	TCT ATC	39 TGA + GAA	O ATG AAA	AGA.	ATA' -+- CGA'	TTC TAT	CTT 	CAA + TAC	AAA GAA	ATC ATT	TAA TGT	AAT	o AGA	TTTTT
	W GGT	D TGC CAG	on AAT + AAA +	6 TTA GTC	ATT CCG	TCT ATC	39 TGA + GAA +	O ATG AAA	AGA. TTG	ATA' -+- CGA'	TTC TAT	CTT AAT	CAA + TAC +	AAA GAA	ATC ATT	TAA TGT	AAT + GAT	AGA	TTTTT + ATGAC
IGAATTGCTGATTGGTCGCAGTTTTCAGTTTAGAGGGAATTTAAAAATCGCCTTTTCGA	W GGT	D TGC CAG	on AAT + AAA +	6 TTA GTC	ATT CCG	TCT ATC	39 TGA + GAA +	ATG	AGA TTG	ATA' -+- CGA' -+-	TTC TAT	CTT	CAA TAC +	AAA GAA	ATC ATT	TAA	AAT + GAT	AGA	TTTTT + ATGAC
IGAATTGCTGATTGGTCGCAGTTTTCAGTTTAGAGGGAATTTAAAAATCGCCTTTTCGA	W GGT	D TGC CAG	on AAT + AAA +	6 TTA GTC t 4	ATT CCG TCG	TCT ATC	39 TGA + GAA +	ATG	AGA TTG	ATA' -+- CGA' -+-	TTC	CTT AAT	CAA + TAC + GGA	AAA GAA 	ATC ATT GTT	TAA TGT	AAT + GAT +	AGA AAA TGG	TTTTT ATGAC
	W GGT	D TGC CAG	on AAT + AAA +	6 TTA GTC t 4	ATT CCG TCG	TCT ATC	39 TGA + GAA +	ATG	AGA TTG	ATA' -+- CGA' -+-	TTC	CTT AAT	CAA + TAC + GGA	AAA GAA 	ATC ATT GTT	TAA TGT	AAT + GAT +	AGA AAA TGG	TTTTT ATGAC
	W I i	D TGC. CAG.	on AAT + AAA + pea TCA	6 TTA GTC t 4	ATT CCG TCG	TCT	39 TGA + GAA +	ATG AAA TCC	AGA TTG TTG GCC	ATA' CGA' -+-	TTC	CTT AAT	CAA + TAC + GGA	AAA GAA TTG	ATC ATT GTT	TAA TGT	AAT + GAT + AAG	AGA AAA TGG	TTTTT+ ATGAC

																							1	A (17	1717)
GG	AG	CG	AA.	AG(c	GTC	CT	GT. +-	AA 	AC	ATT	TTT -+-	AAA 	TGA	TA	AT +-	TAA	TAI	LAT	TTT +	TGC	CAC		LA -+ (
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										1		949	-										•		
GI 	GT	3G?	AG:	AA.	AGA	AC	GCC	GA	GC:	CA 	AG	TG	ACA -+-	TTC	TGA	TT	CG +-	ATA	CGC	AA	CGA	CAC	C:	CA	LA ·+ €
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TA	TG:	rt1	CC	GTC	GA	G <i>I</i>	LAA	CA	GT	GC	TC	TG	GAT	CAT	GGT	TC.	AT	TCA	AGC	CG:	CTC	STG	:AZ	\GT	'G
Y	v	S	3	W	R		N 43	s	+	A	R	G	-+- S	w	F		+- I	Q	A 44	v	+ С	E	:	v	+ 6
						T ((n1	12	9,1	n1	164	1)													
TT	CTC								AT	ΑT	GG	TG:	rtg	TTG.	AGC	TG	CT	GAC	TGA	AG	rca.	ATA	A	SAA	.G
F	s	1		-+- ·H	A		K 45	D	+	 М	D	v	-+- V	E	L	:	+- L	T	E 46	v	N N	ĸ	:	ĸ	+ 6
	7	[(n	24	430)																	A	. (r	124	26)
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v V	A			-+- G	F		Q	T	+	 S			-+-				+-				 -	 E			+]6
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CT 	TG	\AA	CZ	AAA	CA	ΑŢ	GC	AT	GTO	CT.	AAC	TT:	ATT	AGG	ACA	CA	GA.	AAA	ATA	GGC	CAG	\GG	CI	cc	
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								===			- >														
TT 	TGC	AA:	GC	100 -+-	GC.	CG 	CG	CG:	rcz + – -	\A	CC1	`AG	VAT	TTT	\GT	TT:	TT:	AGC	TAA	AAT	[GA]	TG	ÀΊ	TT	
GA	AT	TT	T	TAT	GC.	TA	AT	TT:	rt?	rT(GCG	TT	AA:	rtt'	rga.	AA:	TA	GTC	ACT	ATI	TAT	CG	GG	TT	-
cc	AGI	'AA	A	۸ÀA	TG	TT	TA	TT	A.G.	ÇC.	ATI	'GG	ATT:	AT1	TG	AA	AA	CGA	AAA	TTI	GT;	GT	TI	TT	+ 6 C
AA	CGZ	LAA	T	TA	TC	GA	TT	TT:	ra.	/V.	TGI	'AA'	AA)	LAA.	TA	GC(+ – . GA:	AAA	 TTA	+ CAI	rcaj	·	AT	CA.	+ 6 A
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			•																					•	T (n11
A.	AAA	CA	AG	GG	AT	CG	GT	TT	\GA	T.	TTT	TCC	CCZ	AAZ	TT:	ra?	۱A:	TA	AAT	TTC	AGA	TG	AC	AT	Ċ

FIGURE 4

R	L	L	K 49		· F	` ;	Y	F	W	P	E	A	R	ท 50	s 0	A	V	*		
CT	CGT	GAT'	TCA	TT	GCC	CA	ATI	'GA'	TAA	TT	STCI	GT	TCT	TCT	ccc	CC	GT	CT	CTTI	cec
CA.	ATT	AGT	TTA	AA	ACC	AT	GTG	TA	TAT	TG:	TAI	CC1	ATA	CTC	ATI	TC	CT	TA:	CAT	TCT
\TC	ATT	TCT	CTI	CC	CAI	TT	TCA	CA	CAT	TT	CAT	TT	CTCT	ACG	ATA	ATC	TAI	AAA:	TAT	GAC
TT	TGT	GTC	TCG	AA	CGC	AT	LAA	'AA'	TTT	TA	ATAJ	CTC	GTT	TTG	AAI	TTC	AT:	[AG	rtgi	TGT
:CC	CAG	TAT.	ATA	TG'	TA7	GT	ACI	AT	GCT	TC:	TATO	AAC	AAA	+ ATA	GTI	TC	TAC	GAT	CATC	ACC
CA	ACC	CCA	CCA	AC	CTA	CC	GTA	CC	ATA	TT	CATI	TT	reco	GGG	AAI	CAZ	TT	rcg	ATTA	ATT
TA	ACC	TAT	+ TTI	TT	CGC	CA	CAA	AA	AAT	CT	AAT	TT	rgaa	TTA	ACC	AAT	'AG	CAT	rccc	ATC
CT							_									TTC	GC1	AAT:	PATG	TAT
LAA	TTT	GTA	GGI	cc	ccc	cc	ATC	AT'	TTC	CC	GCC	ATC		TCA	AAI				 TTTT	
 :CG		TAT					-				-			+			-+-			+

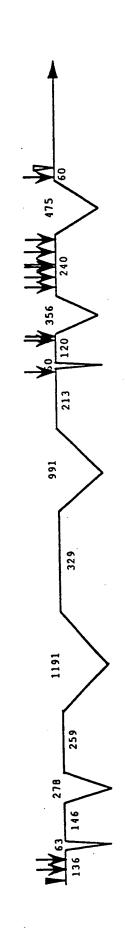


FIGURE 5A

ced-3 Mutations are Clustered

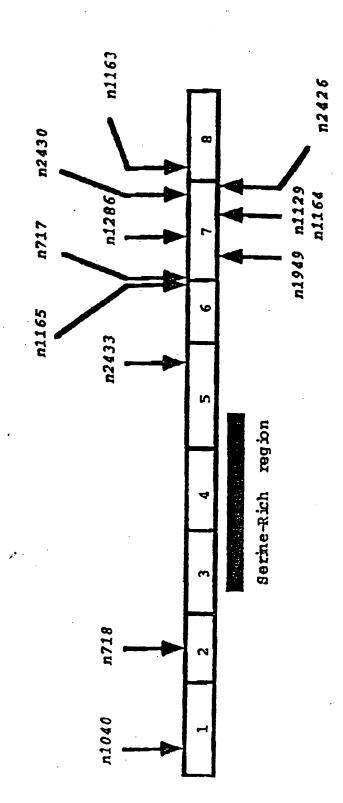
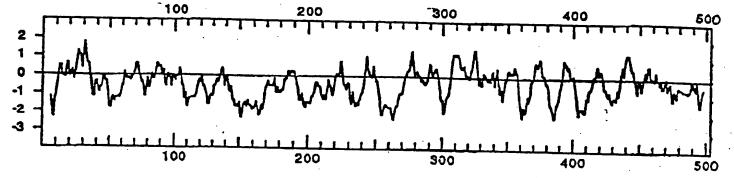


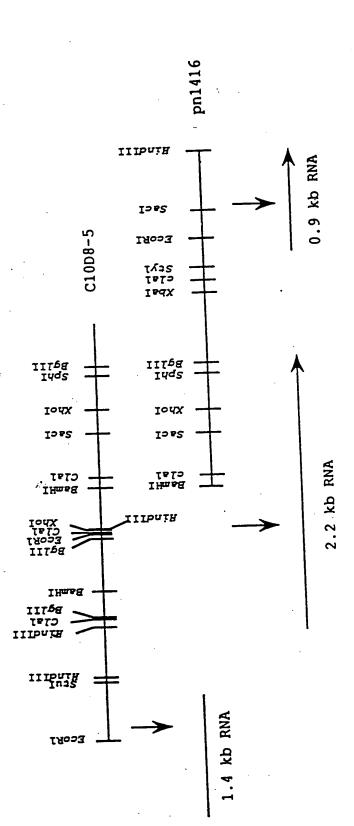
FIGURE 5B



Lines

1 2 3	01	MMRQDRRSLLERNIMMFSSHLKVDEILEVLIAKQVLNSDNGDMINSCGTVWLEK.QA.LDVR.E TVS:SLIR	50
1 2 3	51	REKRREIVKAVQRPGDVAFDAFYDALRSTGHEGLAEVLEPLARSVDSNAV .DNEK	100
1 2 3	101	EFECPMSPASHRRSRALSPAGYTSPTRVHRDSVSSVSSFTS_YQDIYSRA PMSP.AITV S	149
1 2 3	150	RSRSR_SRALHSSDRHNYSSPPVNAFPSQPSSANSSFTGCSSLGYSSSRNSSP.QM.AA_TSA TPTVSS.QAST	198
1 2 3	199	RSFSKASGPTQYIFHEEDMNFVDAPTISRVFDEKTMYRNFSSPRGMCLI 2T.AQSYHLYAHSYHTL	247
1 2 3	248	INNEHFEQMPTRNGTKADKDNLTNLFRCMGYTVICKDNLTGRGMLLTIRDE.SSPISI.HM	297
1 2 3	298	FAKHESHGDSAILVILSHGEENVIIGVDDIPISTHEIYDLLNAANAPRLA .GRNDMVSVNV	347
1 2 3	348	NKPKIVFVQACRGERRDNGFPVLDSVDGVPAFLRRGWDNRDGPLFNFLGCLSLIKG	397
1 2 3	398	VRPQVQQVWRKKPSQADILIRYATTAQYVSWRNSARGSWFIQAVCEVFST	447
1 2 3	448	HAKDMDVVELLTEVNKKVACGFQTSQGSNILKQMPEMTSRLLKKFYFWPE	497
1 2 3	498	ARNSAV 503 DRGDRS	

- Line 1 C. elegans
- Line 2 C. briggsae
- Line 3 C. vulgaris



Σī

nP33JC8 50 kb ced-3 nP35 nP34 MMM-C1 C48D1 W07H4 C43C9 0.5 mu unc-30 C33F2 C37G8 B0564 nP37 C39E9 T10H5 nP36

FIGURE 9

to 1 the building of the water

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Figure 10 Summary of the experiments to localize ced-3 gene within C40D1,

